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Show:

☐ 1: AF366295. Zea mays dihydro-...[gi:14030553]

Links

LOCUS AF366295 1193 bp mRNA linear PLN 14-MAY-2001
DEFINITION Zea mays dihydro-flavanoid reductase-like protein (ms*-bs7) mRNA,
complete cds.

ACCESSION AF366295

VERSION AF366295.1 GI:14030553

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1193)

AUTHORS Fox, T.W., Trimmell, M.R. and Albertsen, M.C.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2001) Trait and Technology Development, Pioneer
Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave. P.O. Box 1004, Johnston, IA
50131-1004, USA

FEATURES

source

Location/Qualifiers

1..1193

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/mol_type="mRNA"

/db_xref="taxon:4577"

gene

1..1193

/gene="ms*-bs7"

CDS

1..996

/gene="ms*-bs7"

/note="anther specific"

/codon_start=1

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/db_xref="GI:14030554"

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VPAVNGTLNVLRSCKKNPFLKRVVLTSSSSAVRIRDDGGQSSNISLDETTWSSVPLCE

KMHLWYALAKVFAEKAWEFAKENGIDLVTVLPSFVIGPSLSHELcVTASDVLGLFQG

DTARFSSYGRMGYVHIDDVASSHILVYEVpQAAGRYLcSSVVLdNDelVSSlAKRYPI

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ORIGIN

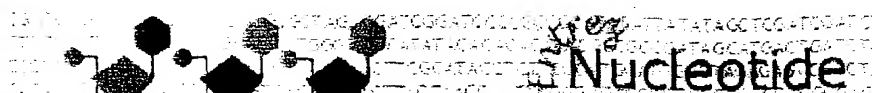
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121 ggaaatcacc aaaaaacagc ccacctttgg aaattacctg gcgctaaaga gaggctgcaa
181 atcgtgagag ctaatctgtt ggaagaaggg agcttcgaca gcgccgtgat ggccgtgtgag
241 ggtgtattcc acactgcatc ccccgctcct gctaaaccgg actctactag caaggaggac
301 acgctcgctc ctgcggtgaa cggtactctg aacgtgctga gatcgtgcaa gaagaacccc
361 ttccctgaaaa gggtcgtcct tacgtcttcg tcgtctgcgg tgaggatcag ggacgacggt
421 ggccagtcga gtaacatctc gctggacgaa acgacatgga gctccgtgcc actctgcgag
481 aagatgcata tatggtatgc ctagccaag gtatttgcag agaaagcggc gtgggagttc
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661 gcaagggttca gctcgtaagg aagaatgggg tacgtccaca tcgacgacgt tgcgagcagc
721 cacatcctgg tgtacgaggt cccccaggcc gccgggaggt acctgtgcag ctcaagtggg
781 ctggacaacg acgagctggg ctccctcgctc gcgaaacgct acccgatatt ccccataccc
841 cggagggtga acagccccta cggcaagcag tcgtaccagc tgaacacgct gaagctgcag
901 gggctgggct tcaagttcag aggggtgcag gagatgttcg acgactgcgt gcagtcgctc
961 aaagaccagg gccacctgct ggagtgcctc ctgtgaactg cgatgggggt gcctcctgtg
1021 aacgcccgtt ttttttttcc ttcaataatt ccacgtcatg tcacgggtgc ctgcgcgaga
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1141 tgtcacgcta gctcgtcatt tgctttgccca tttaaaaaaaa aaaaaaaaaa aaa

//

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 Show:

☐ 1: [AF134807](#). *Oryza sativa* puta...[gi:4581046]

[Links](#)

LOCUS AF134807 1185 bp mRNA linear PLN 07-JUL-1999
 DEFINITION *Oryza sativa* putative dihydroflavonol reductase mRNA, complete cds.
 ACCESSION AF134807
 VERSION AF134807.1 GI:4581046
 KEYWORDS

SOURCE *Oryza sativa*
 ORGANISM *Oryza sativa*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; *Oryza*.

REFERENCE 1 (bases 1 to 1185)
 AUTHORS Zhuang,C.X., Yau,C.P. and Zee,S.Y.
 TITLE Differential expression of a putative dihydroflavonol reductase
 gene in rice (Accession No. AF134807) (PGR 99-074)
 JOURNAL Plant Physiol. 120 (2), 633 (1999)

REFERENCE 2 (bases 1 to 1185)
 AUTHORS Zhuang,C.X., Yau,C.P. and Zee,S.Y.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAR-1999) Department of Botany, The University of
 Hong Kong, Pokfulam Road, Hong Kong

FEATURES
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 CDS 6..998
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 /protein_id="AAD24584.1"
 /db_xref="GI:4581047"
 /translation="MVISSKKGKVCVTGASGFVASWLIKRLLEAGYHVIGTVRDPNRE
 KVSHLWRLPSAKERLQLVRADLMEEGSFDDAVMACEGVFHTASPVLAKS DSNCKEEML
 VPAINGTLNLVLSCKKNPFLKRVVLTSSSSTVRIMDESKHPEISLDETIWSSVALCEK
 LQLWYALAKISAEKAAWEFAKENNIDLTVLPFVIGPSLSHEL SVTASDILGLLQGD
 TDRFISYGRMGYVHIDDVASCHILVYEAPQATGRYLCNSVVL DNNELVALLAKQFPPIF
 PIPRSLRNPYEKQSYELNTSKIQQLGFKFGVQEMFGDCVESLKDQGHLLCPL"

ORIGIN

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121 acccaagcaa tcgcgagaaa gtgtcacacc tttggagatt accaagtgc aaggagaggc
181 tgcaacttgt gagagctgat ctgatggaag aaggagcctt tgacgatgct gtgatggctt
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421 agagtaaaca tccagaaatc tacttgatg aaacaatatg gagctctgtg gcactctgtg
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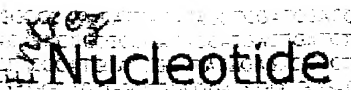
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661 cagatagatt catctcgat gggagaatgg gatatgttca catcgacgat gtggcgagct
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781 ttcttgacaa caacgaatta gtcgccttgc ttgcgaagca atttccaatt tttcccatcc
841 caaggagctt gaggaacca tatgagaaac agtcatatga gctaaacaca tccaagatcc
901 agcagctggg tttcaagttc aaaggggtgc aagagatggt tggtgattgt gtcgagtcgc
961 tgaaagatca gggacacttg ctggagtgc cgttgtaacg aaaaaaaggg atctttggca
1021 cggtagcaac aagctcatgg ccaagcacac acttgaattg ttctgacttt gattcgacac
1081 ttcgcaagcc actgcgtttc tcttgtaata attcgcatgt caattccctc aacaaaacta
1141 caaataaatt gtcaatttgt tgcctcaaaa aaaaaaaaaa aaaaa

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Show: ☐ 1: AA022571. ze72d11.s1 Soares...[gi:1486688]

Links

IDENTIFIERS

dbEST Id: 636653
EST name: ze72d11.s1
GenBank Acc: AA022571
GenBank gi: 1486688
GDB Id: 1281237

CLONE INFO

Clone Id: IMAGE:364533 (3')
Source: IMAGE Consortium, LLNL
DNA type: cDNA

PRIMERS

Sequencing: -40M13 fwd. from Amersham
PolyA Tail: Unknown

SEQUENCE

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AAAAGTTTGGCGATTCTGCTAGCTCTTTTGGGGGCCCAGGCGGCGAAGGCACTGTAGTAT  
CAGTCAGTCCAGGAATATCCTTCTCTCTTTTTTTACAATAACCACTCGTGCCGAATTC  
T
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Quality: High quality sequence stops at base: 398

Entry Created: Aug 9 1996

Last Updated: Aug 9 1996

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

PUTATIVE ID

Assigned by submitter
gb:X67309_rnal 40S RIBOSOMAL PROTEIN S6 (HUMAN);

LIBRARY

Lib Name: Soares_fetal_heart_NbHH19W
Organism: Homo sapiens
Sex: unknown
Organ: heart
Develop. stage: 19 weeks
Lab host: DH10B (ampicillin resistant)

Vector: pT7T3D (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATCTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of normalization
to a Cot = 5. Library constructed by M.Fatima Bonaldo. This
library was constructed from the same fetus as the fetal
lung library, Soares fetal lung NbHL19W.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: The WashU-Merck EST Project
Authors: Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P.,
Wilson, R.
Year: 1995
Status: Unpublished

MAP DATA

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 Show:

☐ 1: CAA75998. dihydroflavonol4-...[gi:3287298]

[BLink](#), [Domains](#), [Links](#)

LOCUS CAA75998 353 aa linear PLN 30-JUN-1998

DEFINITION dihydroflavonol4-reductase [Zea mays].

ACCESSION CAA75998

VERSION CAA75998.1 GI:3287298

DBSOURCE embl locus ZMA1TEOSI, accession Y16042.1

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Bernhardt, J., Stich, K., Schwarz-Sommer, Z.S., Saedler, H. and
 Wienand, U.

TITLE Molecular analysis of a second functional A1 gene
 (dihydroflavonol4-reductase) in Zea mays

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 353)

AUTHORS Wienand, U.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-1997) U. Wienand, Institut fuer Allgemeine
 Botanik, Universitaet Hamburg, Ohnhorststr 18, 22609 Hamburg, FRG

FEATURES

source Location/Qualifiers

1..353

/organism="Zea mays"

/strain="Teosinte guerrero"

/sub_species="parviglumis"

/db_xref="taxon:4577"

Protein

1..353

/product="dihydroflavonol4-reductase"

CDS

1..353

/gene="A1* (second gene), (Teosinte)"

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/db_xref="SPTREMBL:Q9SAN4"

ORIGIN

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181 aaehgldlvs viptlvvgpf lsaamppslv talalvtgne ahysilkqvq fvhlddlcda
241 eiflfepaa agryvcssh d atihglaaml rdrypey dip qklrgiedgl qpvhfsskkl
301 ldhgftfryt vedmfdagir tcrekglip l ataggvgsas lrtptgetdvt nga

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Search for

Limits Preview/Index History Clipboard Details
 Show:

☐ 1: CAA75996. dihydroflavonol4-...[gi:3287294]

[BLink](#), [Domains](#), [Links](#)

LOCUS CAA75996 353 aa linear PLN 30-JUN-1998

DEFINITION dihydroflavonol4-reductase [Zea mays].

ACCESSION CAA75996

VERSION CAA75996.1 GI:3287294

DBSOURCE embl locus ZMA1LINEC, accession [Y16040.1](#)

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Bernhardt, J., Stich, K., Schwarz-Sommer, Z. S., Saedler, H. and
 Wienand, U.

TITLE Molecular analysis of a second functional A1 gene
 (dihydroflavonol4-reductase) in Zea mays

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 353)

AUTHORS Wienand, U.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-1997) U. Wienand, Institut fuer Allgemeine
 Botanik, Universitaet Hamburg, Ohnhorststr 18, 22609 Hamburg, FRG

FEATURES Location/Qualifiers

source 1..353
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 /strain="Line C"
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Protein 1..353
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CDS 1..353
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 Y16040.1:1150..1344,Y16040.1:1476..2045)"
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ORIGIN

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181 aaehgldlvs viptlvvgpf lsaampslv talalvtgne ahysilkqvq fvhlddlcda
241 eiflfepaa agryvcshd atihglaaml rdrypeydp qklrgieddl qpvhfsskkl
301 ldhgftfryt vedmfdagir tcrekglip1 ataggvgsas lrtpgetdvt nga

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Show:

☐ 1: [NP_624490](#). hypothetical prot...[gi:21218711]

[BLink](#), [Domains](#), [Links](#)

LOCUS NP_624490 220 aa linear BCT 02-JUL-2003

DEFINITION hypothetical protein SCJ1.03c [Streptomyces coelicolor A3(2)].

ACCESSION NP_624490

VERSION NP_624490.1 GI:21218711

DBSOURCE REFSEQ: accession NC_003888.3

KEYWORDS complete genome.

SOURCE Streptomyces coelicolor A3(2)

ORGANISM Streptomyces coelicolor A3(2)
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Streptomycineae; Streptomycetaceae; Streptomyces.

REFERENCE 1 (residues 1 to 220)

AUTHORS Bentley,S.D., Chater,K.F., Cerdeno-Tarraga,A.M., Challis,G.L.,
 Thomson,N.R., James,K.D., Harris,D.E., Quail,M.A., Kieser,H.,
 Harper,D., Bateman,A., Brown,S., Chandra,G., Chen,C.W., Collins,M.,
 Cronin,A., Fraser,A., Goble,A., Hidalgo,J., Hornsby,T., Howarth,S.,
 Huang,C.H., Kieser,T., Larke,L., Murphy,L., Oliver,K., O'Neil,S.,
 Rabinowitsch,E., Rajandream,M.A., Rutherford,K., Rutter,S.,
 Seeger,K., Saunders,D., Sharp,S., Squares,R., Squares,S.,
 Taylor,K., Warren,T., Wietzorrek,A., Woodward,J., Barrell,B.G.,
 Parkhill,J. and Hopwood,D.A.

TITLE Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)

JOURNAL Nature 417 (6885), 141-147 (2002)

MEDLINE [21996410](#)

PUBMED [12000953](#)

REFERENCE 2 (residues 1 to 220)

AUTHORS Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,
 Kinashi,H. and Hopwood,D.A.

TITLE A set of ordered cosmids and a detailed genetic and physical map
 for the 8 Mb Streptomyces coelicolor A3(2) chromosome

JOURNAL Mol. Microbiol. 21 (1), 77-96 (1996)

MEDLINE [97000351](#)

PUBMED [8843436](#)

REFERENCE 3 (residues 1 to 220)

AUTHORS Bentley,S.D.

TITLE Direct Submission

JOURNAL Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces
 sequencing team, Sanger Institute, Wellcome Trust Genome Campus,
 Hinxton, Cambridge CB10 1SA E-mail: sdb@sanger.ac.uk

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from [CAB53121](#).
 Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..220
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 /strain="A3(2)"
 /db_xref="taxon:100226"

Protein

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CDS

1..220

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/coded_by="complement (NC_003888.3:144704..145366)"

/note="SCJ1.03c, unknown, len:220 aa, similarity to
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protein TR:P73776 (EMBL: D90909) (218 aa), fasta scores
opt: 291 z-score: 344.1 E(): 8.3e-12 31.2% identity in 170
aa overlap and a weakly similar to Pseudomonas fluorescens
SW:TIPB_PSEFL (EMBL: U44827) thiol:disulfide interchange
protein TipB precursor (cytochrome C biogenesis protein
TipB) (178 aa), fasta scores opt: 148 z-score: 181.8 E():
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/transl_table=11

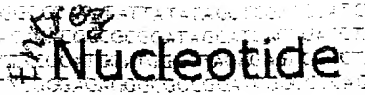
ORIGIN

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121 gsltmaqnd lsydvlsdpq nhigralgiv trptdrvqha qaslglldte vнадgtpdil
181 mptvaivdae gvlrwidvhp nyvtrsepar ilealaravr
```

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dbEST Id: 685952
EST name: mj65g07.r1
GenBank Acc: AA060212
GenBank qi: 1553901

Clone Id: IMAGE:481020 (5')
Source: IMAGE Consortium, LLNL
DNA type: cDNA

Sequencing: -28M13 rev2 from Amersham
PolyA Tail: Unknown

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Quality: High quality sequence stops at base: 395

Entry Created: Sep 23 1996
Last Updated: Sep 23 1996

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

PUTATIVE ID Assigned by submitter
qb:V00714 Mouse gene for alpha-globin (MOUSE);

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Lib Name:      Soares mouse p3NMF19.5
Organism:      Mus musculus
Develop. stage: 19.5 dpc total fetus
Lab host:      DH10B (ampicillin resistant)
Vector:        pT7T3D (Pharmacia) with a modified polylinker
R. Site 1:     Not I

```

R. Site 2: Eco RI
Description: 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of normalization
to a Cot = 5. Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko
(Wayne State University).

SUBMITTER

Name: Marra M/Mouse EST Project
Lab: WashU-HHMI Mouse EST Project
Institution: Washington University School of MedicineP
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: mouseest@watson.wustl.edu

CITATIONS

Title: The WashU-HHMI Mouse EST Project
Authors: Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N.,
Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J.,
Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K.,
Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B.,
Wilson,R., Waterston,R.
Year: 1996
Status: Unpublished

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Show:

☐ 1: [AA050084](#). mj08d06.r1 Soares...[gi:1529754]

Links

IDENTIFIERS

dbEST Id: 665744
EST name: mj08d06.r1
GenBank Acc: AA050084
GenBank gi: 1529754

CLONE INFO

Clone Id: IMAGE:475499 (5')
Source: IMAGE Consortium, LLNL
DNA type: cDNA

PRIMERS

Sequencing: -28M13 rev2 from Amersham
PolyA Tail: Unknown

SEQUENCE

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GGTGTCCGTGTGGAGCAAGGTGCTGCGGACAGACGCGAGCCTGGGACGCATAGCATGCATA
CATCGATGTGATCTACTGGTTCGACAGATCATCGCTCTGGTTTGGGTGTCAATTGGGG
CGTTTTGCCCTTGCGAGGCTTCTTGGGAATAGCAGGATTCTGCCTGATCAATGCAGGAGT
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Quality: High quality sequence stops at base: 417

Entry Created: Sep 9 1996
Last Updated: Sep 9 1996

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:286243

LIBRARY

Lib Name: Soares mouse embryo NbME13.5 14.5
Organism: Mus musculus
Strain: C57BL/6J
Sex: unknown
Tissue type: embryo
Develop. stage: 13.5-14.5dpc total fetus
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI

Description: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGAAATTTTTTTTTTTTTTTTTTTTTTTT 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.

SUBMITTER

Name: Marra M/Mouse EST Project
Lab: WashU-HHMI Mouse EST Project
Institution: Washington University School of MedicineP
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: mouseest@watson.wustl.edu

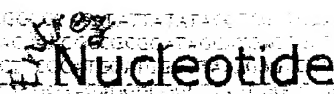
CITATIONS

Title: The WashU-HHMI Mouse EST Project
Authors: Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N.,
Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J.,
Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K.,
Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B.,
Wilson,R., Waterston,R.
Year: 1996
Status: Unpublished

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File

☐ 1: AA060214. mj65h06.r1 Soares...[gi:1553903]

Links

IDENTIFIERS

dbEST Id: 685954
EST name: mj65h06.r1
GenBank Acc: AA060214
GenBank gi: 1553903

CLONE INFO

Clone Id: IMAGE:481019 (5')
Source: IMAGE Consortium, LLNL
DNA type: cDNA

PRIMERS

Sequencing: -28M13 rev2 from Amersham
PolyA Tail: Unknown

SEQUENCE

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GGGAGCTGGGCAGCCTCCCAGAAGGAAAGAGAGTACTCCTGAAACTGAGGAGGGAGCTCC
TACCACCTCAGAGGAAAAGAAGCCAATTCCTGGAATGAAGAAATTTCCAGGACCTGTTGT
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AAATAACAAC

Quality: High quality sequence stops at base: 474

Entry Created: Sep 23 1996
Last Updated: Sep 23 1996

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:291763

LIBRARY

Lib Name: Soares mouse p3NMF19.5
Organism: Mus musculus
Develop. stage: 19.5 dpc total fetus
Lab host: DH10B (ampicillin resistant)
Vector: pT7T3D (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: 1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTACCAATCTGAAGTGGGAGCGCCGATTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University).

SUBMITTER

Name: Marra M/Mouse EST Project
Lab: WashU-HHMI Mouse EST Project
Institution: Washington University School of MedicineP
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: mouseest@watson.wustl.edu

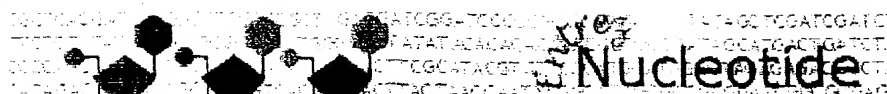
CITATIONS

Title: The WashU-HHMI Mouse EST Project
Authors: Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N.,
Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J.,
Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K.,
Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B.,
Wilson,R., Waterston,R.
Year: 1996
Status: Unpublished

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20

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File

☐ 1: AA060213. mj65h05.r1 Soares...[gi:1553902]

Links

IDENTIFIERS

dbEST Id: 685953
EST name: mj65h05.r1
GenBank Acc: AA060213
GenBank gi: 1553902

CLONE INFO

Clone Id: IMAGE:481017 (5')
Source: IMAGE Consortium, LLNL
DNA type: cDNA

PRIMERS

Sequencing: -28M13 rev2 from Amersham
PolyA Tail: Unknown

SEQUENCE

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GAAAGGCTCTGCTATCACAGGTCCAGTGGCAAAGGAGTGTGCAGACTTGTGGCCCAGAAT
TGCATCCAACGCAGGCAGCATTGCATGATTCTCCAGTGTATTTGTAAAA

Quality: High quality sequence stops at base: 402

Entry Created: Sep 23 1996

Last Updated: Sep 23 1996

COMMENTS

This clone is available royalty-free through LLNL ; contact
the IMAGE Consortium (info@image.llnl.gov) for further
information.
MGI:291761

PUTATIVE ID Assigned by submitter
gb:X52839 60S RIBOSOMAL PROTEIN L17 (HUMAN);

LIBRARY

Lib Name: Soares mouse p3NMF19.5
Organism: Mus musculus
Develop. stage: 19.5 dpc total fetus
Lab host: DH10B (ampicillin resistant)
Vector: pT7T3D (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI

Description: 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University).

SUBMITTER

Name: Marra M/Mouse EST Project
Lab: WashU-HHMI Mouse EST Project
Institution: Washington University School of MedicineP
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: mouseest@watson.wustl.edu

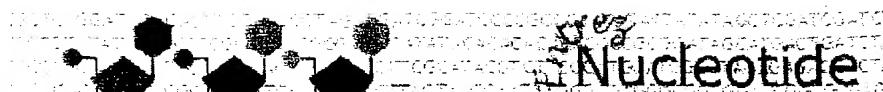
CITATIONS

Title: The WashU-HHMI Mouse EST Project
Authors: Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R., Waterston,R.
Year: 1996
Status: Unpublished

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 Show: ☐ 1: AA053552. z173a01.r1 Strata...[gi:1544505]

Links

IDENTIFIERS

dbEST Id: 679300
EST name: z173a01.r1
GenBank Acc: AA053552
GenBank gi: 1544505
GDB Id: 3813549

CLONE INFO

Clone Id: IMAGE:510216 (5')
Source: IMAGE Consortium, LLNL
DNA type: cDNA

PRIMERS

Sequencing: -28M13 rev2 from Amersham
PolyA Tail: Unknown

SEQUENCE

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CACAGTTGACCAACCCNAAGAGGATCGCCAAGGCCGTGAA

Quality: High quality sequence stops at base: 337

Entry Created: Sep 13 1996
Last Updated: Sep 13 1996

COMMENTS

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

PUTATIVE ID Assigned by submitter
gb:M14328 ALPHA ENOLASE (HUMAN);

LIBRARY

Lib Name: Stratagene colon (#937204)
Organism: Homo sapiens
Organ: colon
Tissue type: tumor
Cell line: T84 carcinoma cell line
Lab host: SOLR cells (kanamycin resistant)
Vector: pBluescript SK-
R. Site 1: EcoRI

R. Site 2: XhoI
Description: Cloned unidirectionally. Primer: Oligo dT. T-84 colonic epithelial cell line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu




CITATIONS

Medline UID: 97044478
Title: Generation and analysis of 280,000 human expressed sequence tags
Authors: Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R., Marra,M.
Citation: Genome Res. 6 (9): 807-828 1996

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1: [AF434703](#). *Triticum monococcum*...[gi:17148808]

Links

LOCUS AF434703 2669 bp DNA linear PLN 20-MAR-2002
DEFINITION *Triticum monococcum* dihydroflavonol-4-reductase gene, complete cds.
ACCESSION AF434703
VERSION AF434703.1 GI:17148808
KEYWORDS
SOURCE *Triticum monococcum*
ORGANISM *Triticum monococcum*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; *Triticum*.

REFERENCE 1 (bases 1 to 2669)
AUTHORS Li, W. and Gill, B.S.
TITLE The colinearity of the sh2/a1 orthologous region in rice, sorghum
and maize is interrupted and accompanied by genome expansion in the
triticeae

JOURNAL Genetics 160 (3), 1153-1162 (2002)

MEDLINE 21898330

PUBMED 11901130

REFERENCE 2 (bases 1 to 2669)
AUTHORS Li, W. and Gill, B.S.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2001) Department of Plant Pathology, Kansas State
University, Throckmorton, Manhattan, KS 66506-5502, USA

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ORIGIN

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2641 ttagcgctct gcagaattga acttgttcc

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ID Q84Z61 PRELIMINARY; PRT; 344 AA.
 AC Q84Z61;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative dihydroflavonol 4-reductase.
 GN P0686C03.24.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
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 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
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 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AP004761; BAC56786.1; -.
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 AC Q9FGH3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Dihydroflavonol 4-reductase-like (Cinnamoyl-CoA reductase-like
 DE protein).
 GN AT5G58490.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
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 RC STRAIN=Columbia;
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 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI";
 RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-Length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
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 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
 RA Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
 RA Ecker J.R., Theologis A.;
 RT "Arabidopsis Open Reading Frame (ORF) Clones.";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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 DR EMBL; AY086975; AAM64538.1; -.
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 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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 RX MEDLINE=99372458; PubMed=10447467;
 RA Zhuang C.X., Yau C.P., Zee S.Y.;
 RT "Differential expression of a putative dihydroflavonol reductase gene
 RT in rice (Accession No. AF134807) (PGR 99-074).";
 RL Plant Physiol. 120:633-633(1999).
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 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
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 RN [1]
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 RA Fox T.W., Trimnell M.R., Albertsen M.C.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
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 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
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 DE reductase).
 GN ANT18.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
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 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Gula;
 RX MEDLINE=92079919; PubMed=1720864;
 RA Kristiansen K.N., Rohde W.;
 RT "Structure of the Hordeum vulgare gene encoding dihydroflavonol-4-
 RT reductase and molecular analysis of ant18 mutants blocked in
 RT flavonoid synthesis.";
 RL Mol. Gen. Genet. 230:49-59(1991).
 CC -!- CATALYTIC ACTIVITY: CIS-3,4-LEUCOPELARGONIDIN + NADP(+) = (+)-
 CC DIHYDROKAEMPFEROL + NADPH.
 CC -!- PATHWAY: FLAVONOID SYNTHESIS; ANTHOCYANIDINS BIOSYNTHESIS.
 CC -!- SIMILARITY: BELONGS TO THE DIHYDROFLAVONOL-4-REDUCTASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
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 DR EMBL; S69616; AAB20555.1; -.
 DR PIR; S18595; S18595.
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Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Boo

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1: S69616. Ant18=dihydroflav...[gi:240051]

Links

LOCUS S69616 3193 bp DNA linear PLN 07-MAY-1993

DEFINITION Ant18=dihydroflavonol-4-reductase [Hordeum vulgare=barley, cv. Gula, Genomic, 3193 nt].

ACCESSION S69616

VERSION S69616.1 GI:240051

KEYWORDS

SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 3193)

AUTHORS Kristiansen, K.N. and Rohde, W.

TITLE Structure of the Hordeum vulgare gene encoding dihydroflavonol-4-reductase and molecular analysis of ant18 mutants blocked in flavonoid synthesis

JOURNAL Mol. Gen. Genet. 230 (1-2), 49-59 (1991)

MEDLINE 92079919

PUBMED 1720864

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 69616] from the original journal article. This sequence comes from 5.

FEATURES

Location/Qualifiers

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Nov 3 2003 07:26:36

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 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Dihydroflavonol-4-reductase.
 OS Triticum monococcum (Einkorn wheat) (Small spelt).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 OC Triticeae; Triticum.
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 RA Li W., Gill B.S.;
 RT "Colinearity of the Sh2/A1 region among rice, sorghum and maize is
 RT interrupted and accompanied by genome expansion in the Triticeae.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Entrez PubMed Nucleotide Protein Genome Structure PMC Taxonomy Books

Search for

Display Limits Show: Preview/Index History

☐ 1: Y16042. Zea mays Al* gene...[gi:3287297]

Links

LOCUS ZMA1TEOSI 2174 bp DNA linear PLN 30-JUN-1998

DEFINITION Zea mays Al* gene (second), strain Teosinte guerrero.

ACCESSION Y16042

VERSION Y16042.1 GI:3287297

KEYWORDS Al gene; dihydroflavonol 4-reductase.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1

AUTHORS Bernhardt, J., Stich, K., Schwarz-Sommer, Z.S., Saedler, H. and
Wienand, U.

TITLE Molecular analysis of a second functional Al gene
(dihydroflavonol 4-reductase) in Zea mays

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2174)

AUTHORS Wienand, U.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-1997) U. Wienand, Institut fuer Allgemeine
Botanik, Universitaet Hamburg, Ohnhorststr 18, 22609 Hamburg, FRG

FEATURES Location/Qualifiers

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